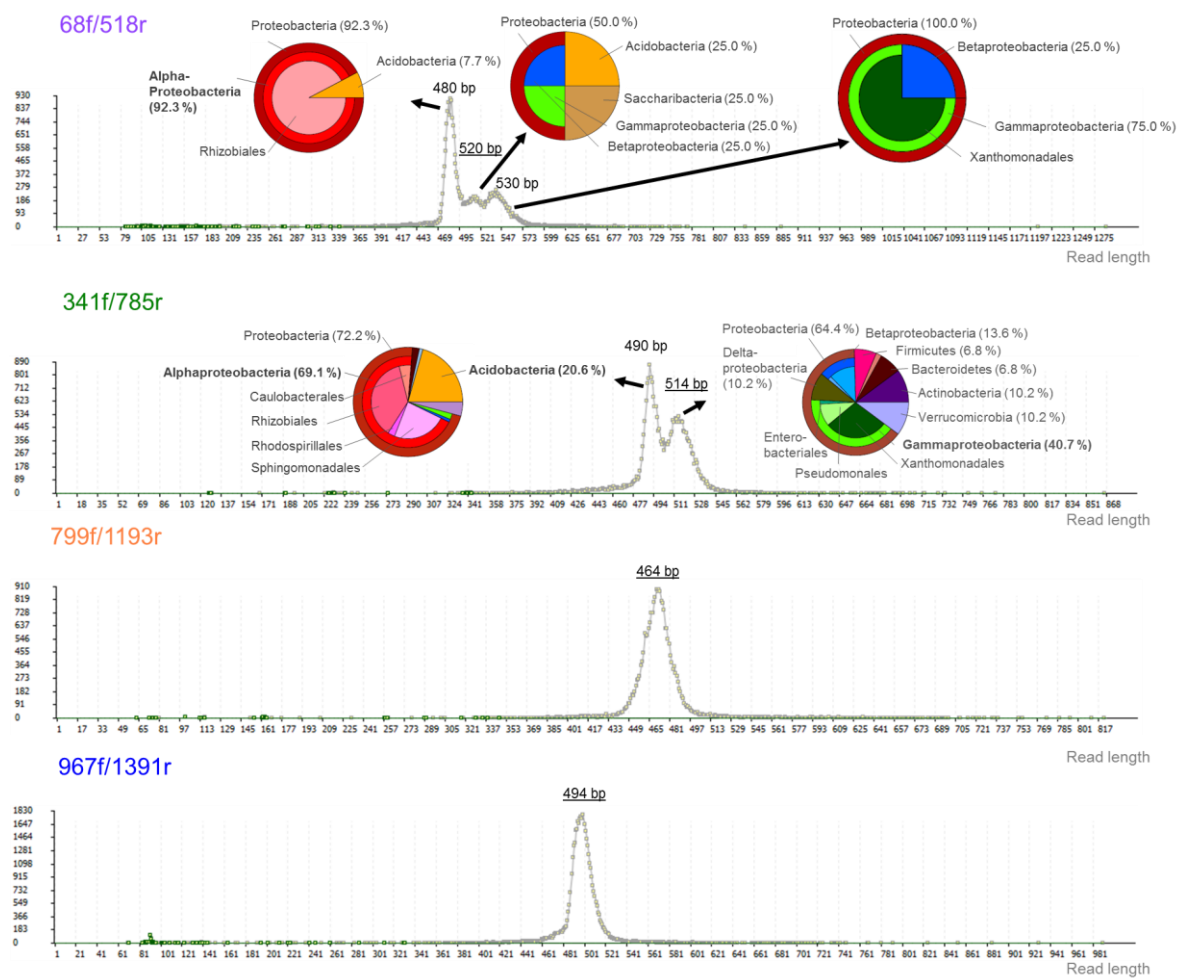
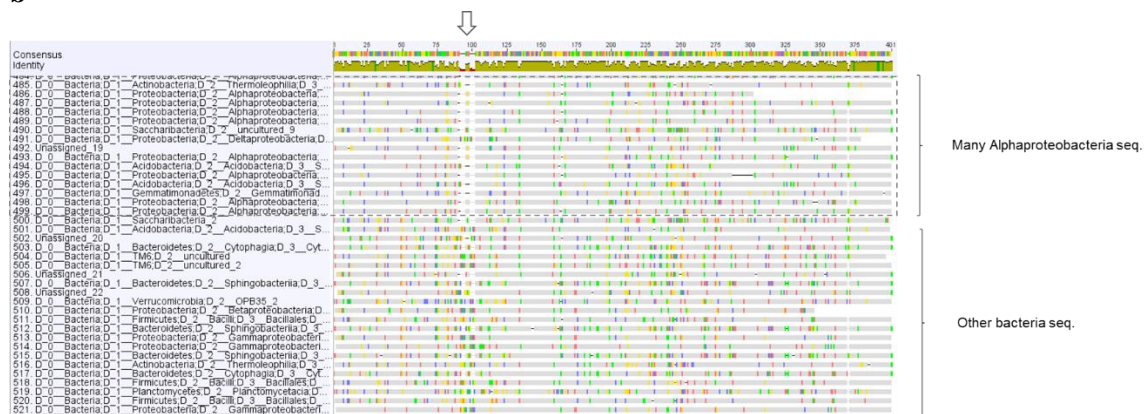


**a**



**b**



**Supplementary Figure 2: Raw sequence length distribution per primer pair and multiple sequence alignment.** Graphs show the raw 16S rRNA gene sequences for each primer pair as generated by pyrosequencing of the bulk soil and *Acer pseudoplatanus* rhizosphere soil samples collected from a military forest, Zwijndrecht, Belgium (**a**). Pie charts show the taxonomic distribution of 1,000 randomly picked quality filtered 16S sequences blasted against the SILVA v123 database. The picture at the bottom shows a snapshot of the multiple sequence alignment of 1,000 randomly picked 16S sequences from the 490 bp peak and 514 bp peak of 341f/785r (**b**). The arrow indicates the gaps in the 16S sequence at positions 454-465 and 476-485 (*E. coli* numbering) in Alphaproteobacteria whereas this was not detected in other bacterial taxa.